GENIC-CYTOPLASMIC INTERACTIONS AFFECTING GROWTH HABIT IN PEANUTS, *A. HYPOGAEA* II. A REVISED MODEL

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THERE are two distinct growth habits in peanuts (*A. hypogaea* L.), runner (trailing) and bunch (erect). In a previous paper (ASHRI 1964) a model of genic-cytoplasmic interactions producing these growth habit differences was advanced. Since then the model has been tested with derived lines which facilitated critical examination of certain points that at the time could not be verified. The results show that one of the previous interpretations should be revised.

MATERIALS AND METHODS

The two varieties used in this study were described in detail earlier (ASHRI 1964). The Israeli variety V4 (full name—Virginia Beit Dagan No. 4) is the only one identified so far as having one of the plasmon types, called [V4], is $Hb_1Hb_1hb_2hb_2$ and is bunch. The second variety, G2 (Virginia Bunch G2) was introduced from the U.S.A. It is one of several other varieties having the second plasmon type designated ["Others"], is $hb_1hb_1Hb_2Hb_2$ and is also bunch. F_4 plants from true breeding runner (TBR) F_3 lines derived from reciprocal crosses of the two varieties were hybridized in various combinations. The TBR plants with the [V4] plasmon were progenies of the F_3 plant No. 1963-375-2 from the cross ($V_4 \text{♀} \times G2 \text{♂}$). Those with the ["Others"] plasmon were progenies of F_3 plant No. 1963-439-2 from the cross ($G2 \text{♀} \times V4 \text{♂}$).

The field procedures, handling and classification methods were as described previously (ASHRI 1964).

RESULTS AND DISCUSSION

Alternative models: The previous model with two plasmon types and two genes is shown in Table 1. Briefly, it called for complementary action of Hb_1 and Hb_2 to produce a runner plant in the [V4] plasmon. All genotypes not containing at least one dominant allele of each of the two genes would be bunch in this plasmon. In the ["Others"] cytoplasm the dominants Hb_1 and Hb_2 or the recessives hb_1 and hb_2 were shown to be additive. It was suggested that when only one dominant allele was present, Hb_1 or Hb_2 or neither, the plants were runner. Stated differently, in the ["Others"] plasmon runner plants would result from the action of 3 or 4 of the recessive alleles hb_1 and hb_2 in any combination. According to that model, it was proposed that in the ["Others"] plasmon bunch plants would be those having 2 or more dominant alleles in any combination (see Table 1).

Another model of the interactions is possible and it is also shown in Table 1. This model calls for complementary gene action in the [V4] plasmon as before.

TABLE 1

The initial (I) and revised (II) models of genic interactions in and with the two plasmon types

Parents: Bunch [V4] $Hb_1Hb_1hb_2hb_2$ $\times$ ["Others"] $hb_1hb_1Hb_2Hb_2$ bunch

F₁: $Hb_1hb_1Hb_2hb_2$ runner in [V4] plasmon

bunch in ["Others"] plasmon

F ₂ genotypes	F ₂ phenotypes in plasmons of			
	[V4]		["Others"]	
	Models I and II	Model I	Model II	
$Hb_1Hb_1Hb_2Hb_2$ 1/16	runner	bunch	runner	5/16
$Hb_1Hb_1Hb_2hb_2$ 2/16	runner	bunch	runner	
$Hb_1hb_1Hb_2Hb_2$ 2/16	runner	bunch	runner	
	9/16			
$Hb_1hb_1Hb_2hb_2$ 4/16	runner	bunch	11/16 bunch	11/16
$Hb_1Hb_1hb_2hb_2$ 1/16	bunch	bunch	bunch	
$hb_1hb_1Hb_2Hb_2$ 1/16	bunch	bunch	bunch	
	7/16			
$Hb_1hb_1hb_2hb_2$ 2/16	bunch	runner	bunch	5/16
$hb_1hb_1Hb_2hb_2$ 2/16	bunch	runner	bunch	
$hb_1hb_1hb_2hb_2$ 1/16	bunch	runner	bunch	

However, in the ["Others"] plasmon, rather than to assume that the recessive alleles are additive, it is postulated that the dominant alleles are additive (and possibly complementary); i.e., $Hb_1Hb_1Hb_2hb_2$, $Hb_1hb_1Hb_2Hb_2$ and $Hb_1Hb_1Hb_2Hb_2$ are runner and all other genotypes are bunch.

Breeding tests which are customarily employed, such as the behavior of F₃ lines, BC₁F₁ (first generation after a backcross) and BC₁F₂ populations do not differentiate between the two models. The F₃ expectations in the ["Others"] plasmon (wherein the models differ) would be the same with both models. BC₁F₁ expectations in the ["Others"] plasmon are again the same with both models, 3 bunch:1 runner, and BC₁F₂ populations are also expected to behave in the same manner with both models. The same is true for reciprocal backcrosses of the F₁ hybrids to either parent type.

TBR $\times$ TBR cross. A critical evaluation of the two models can be obtained by crossing derived, advanced generation TBR lines having the two cytoplasms. According to the first model (Table 1) the cross and expectations would be:

TBR; [V4] $Hb_1Hb_1Hb_2Hb_2$ φ $\times$ TBR; ["Others"] $hb_1hb_1hb_2hb_2$ δ

↓

F₁; [V4] $Hb_1hb_1Hb_2hb_2$, runner

↓

F₂; [V4], segregating 9 runner:7 bunch.

With the second model (Table 1) the cross and expectations would be:

TBR; [V4] $Hb_1Hb_1Hb_2Hb_2$ φ $\times$ TBR; ["Others"] $Hb_1Hb_1Hb_2Hb_2$ δ

↓

F₁; [V4] $Hb_1Hb_1Hb_2Hb_2$, runner

↓

F₂; [V4], no segregation, all runner

Such a cross was made and 4 F_1 plants were obtained, all runners. In the F_2 there was no segregation, all 154 plants grown were runner. Thus it must be concluded from this test that the second alternative holds, and that model II detailed in Table 1 should be adopted.

G2 × TBR, [V4] plasmon cross: Another critical evaluation of the two models would result from crossing G2 as female with a TBR, [V4] plasmon. According to the first model (Table 1) the expectations would be:

$$\begin{array}{c} G2; ["Others"] \text{ } hb_1hb_1Hb_2Hb_2 \text{ } \varnothing \times TBR; [V4] \text{ } Hb_1Hb_1Hb_2Hb_2 \text{ } \delta \\ \downarrow \\ F_1; ["Others"] \text{ } Hb_1hb_1Hb_2Hb_2, \text{ bunch} \\ \downarrow \\ F_2; ["Others"], \text{ no segregation, all bunch} \end{array}$$

Following the second model (Table 1) the results should be:

$$\begin{array}{c} G2; ["Others"] \text{ } hb_1hb_1Hb_2Hb_2 \text{ } \varnothing \times TBR; [V4] \text{ } Hb_1Hb_1Hb_2Hb_2 \text{ } \delta \\ \downarrow \\ F_1; ["Others"] \text{ } Hb_1hb_1Hb_2Hb_2, \text{ runner} \\ \downarrow \\ F_2; ["Others"], \text{ segregating 3 runner:1 bunch} \end{array}$$

This cross was performed and the 4 F_1 plants grown were runner. The F_2 segregated 76 runner:29 bunch; goodness of fit to a 3:1 ratio $\chi^2 = 0.46$, $P = 0.50-0.30$. Progeny tests in the F_3 verified the F_2 results: 9 bunch F_2 plants gave only bunch offspring. 21 runner F_2 plants were progeny tested, 7 gave only runner progenies, while 14 gave offspring which segregated 3:1 in accordance with the monogenic segregation pattern expected. The fact that in this cross the F_1 plants were runner and the F_2 segregated support the second model.

TBR, [V4] plasmon × V4 hybrids: This cross can be used to verify the genic constitution of V4 and the other varieties, formerly deduced by intervarietal hybridization. According to both models the genotype of a TBR with [V4] plasmon is $Hb_1Hb_1Hb_2Hb_2$ while V4 plants are homozygous dominant for one locus and recessive for another. Arbitrarily they were designated $Hb_1Hb_1hb_2hb_2$. F_1 hybrids of the two should be $[V4] \text{ } Hb_1Hb_1Hb_2hb_2$ and runner; the F_2 should segregate 3 runner:1 bunch. This cross yielded 4 runner F_1 plants and the F_2 segregated 40 runner:12 bunch, goodness of fit for a 3:1 ratio $\chi^2 = 0.103$, $P = 0.80-0.70$. F_3 progeny testing verified the monogenic difference between the derived TBR line and V4. Thus, V4 is $Hb_1Hb_1hb_2hb_2$ and it follows that G2 and several other varieties are $hb_1hb_1Hb_2Hb_2$.

SUMMARY

Data are presented supporting previous findings that two plasmons and two genes interact to produce the runner (trailing) or bunch (erect) growth habit in peanuts. The results indicate that the dominant alleles Hb_1 and Hb_2 lead to the development of a runner habit in both plasmons. In the [V4] plasmon they are complementary, with Hb_1-Hb_2- being runner and all other genotypes being bunch. In the ["Others"] plasmon, however, the dominant alleles are additive

and perhaps also complementary. At least 3 dominant alleles, in any combination, are required to produce a runner; with 2, 1, or 0 dominant alleles the plants are bunch in this plasmon. Thus, $Hb_1Hb_1Hb_2Hb_2$, $Hb_1Hb_1Hb_2hb_2$ and $Hb_1hb_1Hb_2Hb_2$ are runner in the ["Others"] plasmon, while all other genotypes are bunch.

LITERATURE CITED

- ASHRI, A., 1964 Intergenic and genic-cytoplasmic interactions affecting growth habit in peanuts. *Genetics* **50**: 363-372.